

Application No.: 09/677,752
Amendment Dated: February 17, 2006
Reply to Office Action of: August 30, 2005

Attorney Docket No.: 71515.087.999
Customer No.: 35161

REMARKS

This Amendment is in response to the Office Action mailed on August 30, 2005, for the present application, which has been reviewed. Considered together with the following remarks, the arguments below and request for reconsideration are believed sufficient to place the application into condition for allowance. No new matter has been added to the application. Applicants express appreciation for the thoughtful examination by the Examiner.

Support for the amendments can be found in the specification as follows:

Amendment to claim 108:	page 18, Table 1.
Amendment to claim 130:	page 21, lines 20-34.

The present invention is drawn to PMP polypeptides of *Chlamydia*, further defined by amino acid and nucleotide sequences thereof, used in vaccine formulations comprising an effective amount of said polypeptide.

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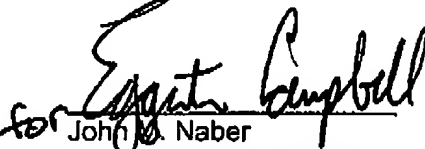
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CONCLUSION

In light of the foregoing, Applicants respectfully submit they have addressed each and every item presented by the Examiner in this Office Action. Favorable reconsideration of all of the claims as amended is earnestly solicited. Applicants submit that the present application, with the foregoing claim and specification amendments and accompanying remarks, is in a condition for allowance and respectfully request such allowance.

In the event any further matters requiring attention are noted by Examiner or in the event that prosecution of this application can otherwise be advanced thereby, a telephone call to Applicants' undersigned representative at the number shown below is invited.

Respectfully submitted,


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Date: February 17, 2006

DC 71515-07 108702v2 2/17/2006

Thursday, September 8, 2001

Blast Result

Page: 1



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☒ Align

Sequence 1 kclseq_1 Length 956 (1..956)

Sequence 2 kclseq_2 Length 965 (1..965)



Score and expect value) is calculated based on the size of nr database

Score = 1885 bits (4884), Expect = 0.0
Identities = 925/934 (99%), Positives = 930/934 (99%)

Query: 23 VPDPTKESLSNKISLTGOTHNLNLCYLDNLRYILAILQKTPNEGAAVTITDYLSPFDQK 82
Sbjct: 32 VPDPTKESLSNKISLTGOTHNLNLCYLDNLRYILAILQKTPNEGAAVTITDYLSPFDQK 91

Query: 83 EGIYFAKNLTPESGGAIGYASPNSTVEIRDITIGPVIFENNTCCRPFTSSNPNAAVVKIR 142
Sbjct: 92 EGIYFAKNLTPESGGAIGYASPNSTVEIRDITIGPVIFENNTCCRPFTSSNPNAAVVKIR 151

Query: 143 EGGAIHAQNLYINHHNDVVGFMKNFSYVRGGAISTANTFVVSENQSCFLFMDNICIQNT 202
Sbjct: 152 EGGAIHAQNLYINHHNDVVGFMKNFSYVRGGAISTANTFVVSENQSCFLFMDNICIQNT 211

Query: 203 AGKGGAIYAOTSNSFESNNDLFFINNACAGGAI FSPICSLTGNRGNI VYNNRCFQIV 262
Sbjct: 212 AGKGGAIYAOTSNSFESNNDLFFINNACAGGAI FSPICSLTGNRGNI VYNNRCFQIV 271

Query: 263 ETASSEASDGGAIKVTRLDTGNRGRIFSDNITKNYGGAIYAPVVTLVNQGPTYPINN 322
Sbjct: 272 ETASSEASDGGAIKVTRLDTGNRGRIFSDNITKNYGGAIYAPVVTLVNQGPTYPINN 331

Query: 323 VANKGGAIYIDGTNSKISADRHAIIFNENIVTNVTANOTSTSANPFRNAITVASS 382
Sbjct: 332 IANKGGAIYIDGTNSKISADRHAIIFNENIVTNVTANOTSTSANPFRNAITVASS 391

Query: 383 GEILLGAGSSQNLIFYDPIEVSNAGVSVPNKEADQTGVSVPFGATVNSADPHQNLQTK 442
Sbjct: 392 GEILLGAGSSQNLIFYDPIEVSNAGVSVPNKEADQTGVSVPFGATVNSADPHQNLQTK 451

Query: 443 TPAPLTLENGFLCIEDHAQLTVNRFTQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH 502
Sbjct: 452 TPAPLTLENGFLCIEDHAQLTVNRFTQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH 511

Query: 503 IGLKLSSTLKSGAETPLMVEPTNENNYTADTAATFSLSDVKLSLIDYGNSPYESTDL 562
Sbjct: 512 IGLKLSSTLKSGAETPLMVEPTNENNYTADTAATFSLSDVKLSLIDYGNSPYESTDL 571

day, September 6, 2001

Blast Result

Page: 2

Query: 512 IGLNLSSILKSGAEIPLWVEPTNNSNNTADTAATFSLSDVKLSLIDYGNSESTDL 571
Query: 563 THALSSQPMLSISEASDNQLRSDDMDFSGLNVPHYGWQGLNSWGWAKTQDPEPASSATIT 622
THALSSQPMLSISEASDNQLRSDDMDFSGLNVPHYGWQGLNSWGWAKTQDPEPASSATIT
Query: 572 THALSSQPMLSISEASDNQLRSDDMDFSGLNVPHYGWQGLNSWGWAKTQDPEPASSATIT 631
Query: 623 DPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTFSDFPF 682
DPK+KANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTFSDFPF
Query: 632 DPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTFSDFPF 691
Query: 693 WGITGGGLGMVYQEPRENHPGFHRSSTGYAGMIAGQTHTFSLKFSQTYTKLNERYAKN 742
WGITGGGLGMVYQEPRENHPGFHRSSTGYAGMIAGQTHTFSLKFSQTYTKLNERYAKN
Query: 692 WGITGGGLGMVYQEPRENHPGFHRSSTGYAGMIAGQTHTFSLKFSQTYTKLNERYAKN 751
Query: 743 NVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFTYQGENLTSQGTFRSQTMGG 802
NVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFTYQGENLTSQGTFRSQTMGG
Query: 752 NVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFTYQGENLTSQGTFRSQTMGG 811
Query: 803 AVFFDLPMKPFQSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINLVPIGVK 862
AVFFDLPMKPFQSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINLVPIGVK
Query: 812 AVFFDLPMKPFQSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINLVPIGVK 871
Query: 863 GSFNATQRPQAWTVELAYQPVLRYQELIATQLLASKGIWFGSGSPSSRHAMSYSKISQQ 922
GSFNATQRPQAWTVELAYQPVLRYQELIATQLLASKGIWFGSGSGSPSSRHAMSYSKISQQ
Query: 872 GSFNATQRPQAWTVELAYQPVLRYQELIATQLLASKGIWFGSGSGSPSSRHAMSYSKISQQ 931
Query: 923 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 956
TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
Query: 932 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 965

PU time: 0.36 user secs. 0.02 sys. secs 0.38 total secs.

apped
ambda K H
0.316 0.132 0.396

apped
ambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12,524

Number of Sequences: 0

Number of extensions: 873

Number of successful extensions: 15

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

Length of query: 956

Length of database: 239,316,239

Effective HSP length: 131

Effective length of query: 825

Effective length of database: 206,523,009

Effective search space: 170381482425

Effective search space used: 170381482425

r: 9

A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 77 (34.3 bits)